



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

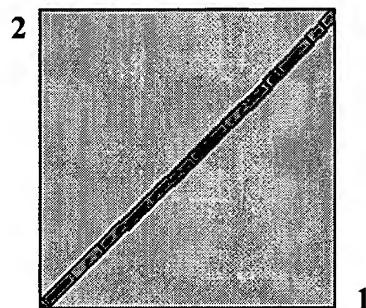
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix **BLOSUM62** ▼ gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0** wordsize: **3** Filter Align

Sequence 1 lcl|seq_1 Length 751 (1 .. 751)

Sequence 2 lcl|seq_2 Length 771 (1 .. 771)

Sema E
Sema D



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 708 bits (1827), Expect = 0.0
 Identities = 339/757 (44%), Positives = 508/757 (66%), Gaps = 17/757 (2%)



Query: 4 RTICVLGVFICSIC-VKGSSQPQARVYLTDELRETKTSEYFSLSHHPLDYRILLMDDED 62
 R +C+ GV ++ + R+ L++ E+ E+ F+ + Y L+DE+
 Sbjct: 6 RIVCLFWGVLLTARANYQNGKNNVPRLKLSYKEMLESNNVITFNGLANSSSYHTFLLDEE 65

Query: 63 QDRIYVGSKDHILSLNINNISQEALSVFWPASTIKVEECKMAGKDPTHGCGNFVRVIQTF 122
 + R+YVG+KDHIS++ NI ++ + WP S + +ECK AGKD C NF++V++ +
 Sbjct: 66 RSRLYVGAKDHIFSFDLVNI-KDFQKIVWPVSYTRDECKWAGKDILKECANFIKVLKAY 124

Query: 123 NRTHLYVCGSGAFSPVCTYLNRRGRRSEDQVFMD-SKCESGKGRCSFNPNVNTVSVMINE 181
 N+THLY CG+GAF P+CTY+ G ED +F ++ S E+G+G+ ++P + T S++I+
 Sbjct: 125 NQTHLYACGTGAFHPICTYIEIGHHPEDNIFKLENSHFENGGRGKSPYDPKLLTASLLIDG 184

Query: 182 ELFSGMYIDFMGTDAAIFRSLTKRNAVRTDQHNSKWLSPEMFVDAVIPDGTDPNDAKVV 241
 EL+SG D DF MG D A IF R+L + +RT+QH+S+WL++P F+ AH+I + +P D KVY
 Sbjct: 185 ELYSGTAADFMGRDFAIFRTLGHHHPIRTEQHDSRWLNDPKFISAHLISESDNPEDDKVV 244

Query: 242 FFFKEKLTDNNRSTKQIHSMIARI CPNDTGGRLSLVNWKTTFLKARLVC SVTDEDG PETH 301
 FFF+E D S K H+ I +IC ND GG RSLVNWKTTFLKARL+CSV +G +TH
 Sbjct: 245 FFFRENAIDGEHSGKATHARIGQICKNDFGGHRSLVNKTTFLKARLIC SVPGP PNGIDTH 304

Query: 302 FDELEDVFLLETDNPRTTLVYGIFTSSSVFKGSAVCVYHLSDIQTVFNGPFAHKEGPNH 361
 FDEL+DVFL+ +P+ +VYG+F TTSS++FKGSAVC+Y +SD++ VF GP+AH++GPN+
 Sbjct: 305 FDELQDVFLMNFKDPKNPVYGVFTTSSNIFKGSAVCMYMSDVRVFLGPYAH RDGP NY 364

Query: 362 QLISYQGRIPYPRPGTCPGGAFTPNMRTTKEFPDDVVT FIRNHPLMYNSIYPIHKRPLIV 421
 Q + YQGR+PYPRPGTCP F +TK+ PDDV+TF R+HP MYN ++P++ RP+++
 Sbjct: 365 QWVPYQGRVPYPRPGTCPSKTF-GGF DSTKDLPPDDVITFARSHPAMYNPV FPMNNRPIVI 423

Query: 422 RIGTDYKYTKIAVDRVNAADGRYHVLFLGTDRTVQKVVVLPTNNVS -GELILEELEV 480
 + +Y++T+I VDRV+A DG+Y V+F+GTD GTV KVV +P E++LEE+ VF
 Sbjct: 424 KTDVNQFTQIVVDRVDAEDGQYDVMFIGTDVGTVLKVVSIKPETWYDLEEVILLEEMTVF 483

Query: 481 KNHAPITTMKISSKKQQQLYVSSNEGVSQVSLHRCHIYGTACADCLARDPYCAWDGHSCS 540
 + I+ M++S+K+QQLY+ S GV+Q+ LHRC IYG ACA+CCLARDPYCAWDG +CS
 Sbjct: 484 REPTAISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYKGKACAECCLARDPYCAWDGSACS 543

Query: 541 RFYPTGKRRSRRQDVHGNPLTCRGNFLKAY--RNAAEIVQYGVKNNTTFLECAPKSPQ 598
 R++PT KRR+RRQD+R+G+PLT C + + + E + YGV+N++TFLEC+PKS +
 Sbjct: 544 RYFPTAKRRTRRQDIRNGDPLTHCSDLHHHDNHHGHSPEERIIYGVENSSTFLECPKSQR 603

Query: 599 ASIKWLLQ-KDKDRRKEVKLNERIIATSGLLIRSVQGSDQGLYHCIATENSFKQTIAKI 657
 A + W Q +++++R++E+++++ II T QGLL+RS+Q D G Y C A E+ F QT+ K+
 Sbjct: 604 ALVYWQFQRRNEERKEEIRVDDHIIRTDQGLLRLSLQQKDSGNYLCHAVEHGFIQTLLKV 663

Query: 658 NFKVLDSEMVAVTDKWSPWTWA-----SSVRALPFHPKDIMGAFSHSEMQMINYCK 710
 +V+D+E + + K + + S + +D M +H + +++++C+
 Sbjct: 664 TLEVIDTEHLEELLHKDDDGDGSKTKEMSNSMTPSQKVWYRDFMQLINHPNLNTMDEFCE 723

Query: 711 DT--RQQHQQGDESQKMRGDYGKLKALINSRKSRR 745
 R + Q+ G+ K K L ++K RNRR
 Sbjct: 724 QVWKRDRKQRRQRPGHTPGNSNKWHLQENKKGRNRR 760

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.

Lambda	K	H
0.321	0.135	0.413

Gapped		
Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 4866
 Number of Sequences: 0
 Number of extensions: 399
 Number of successful extensions: 8
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0
 Number of HSP's gapped (non-prelim): 1
 length of query: 751
 length of database: 479,146,392
 effective HSP length: 135
 effective length of query: 616
 effective length of database: 479,146,257
 effective search space: 295154094312
 effective search space used: 295154094312
 T: 9
 A: 40
 X1: 16 (7.4 bits)
 X2: 129 (49.7 bits)
 X3: 129 (49.7 bits)
 S1: 41 (21.8 bits)
 S2: 79 (35.0 bits)